Figure 1.
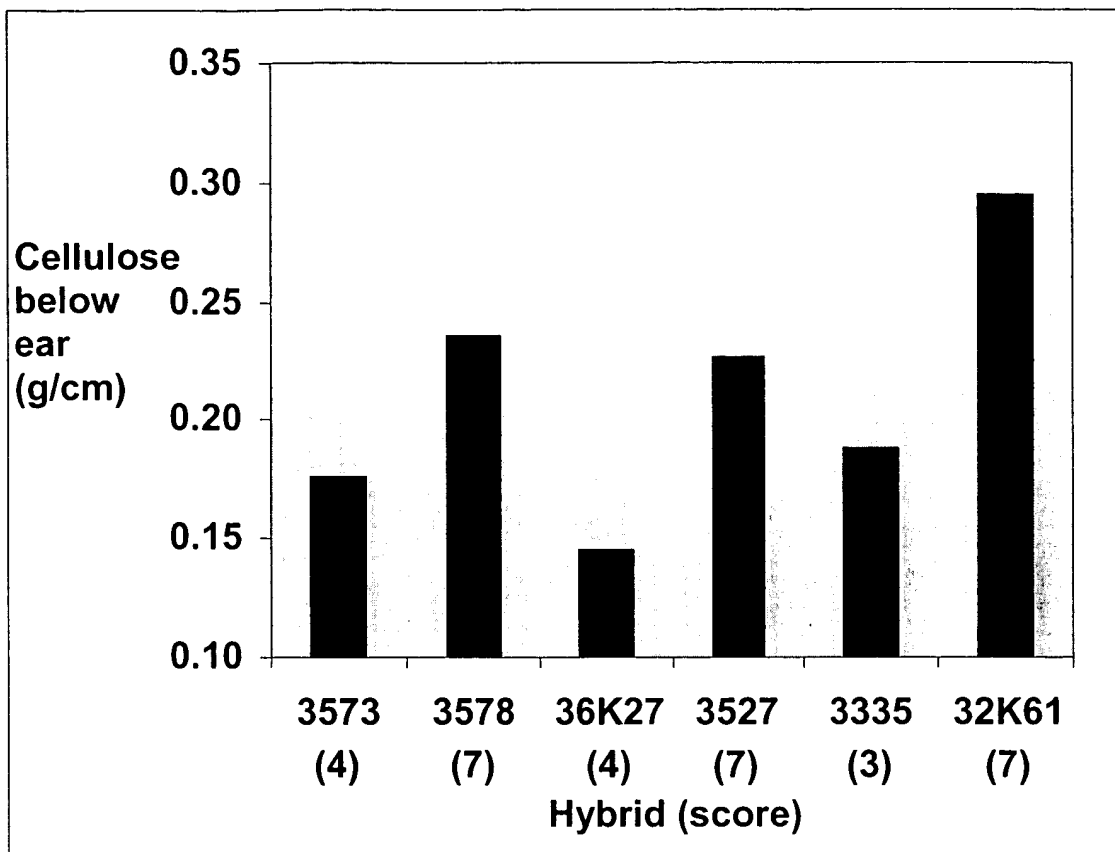
Figure 2.
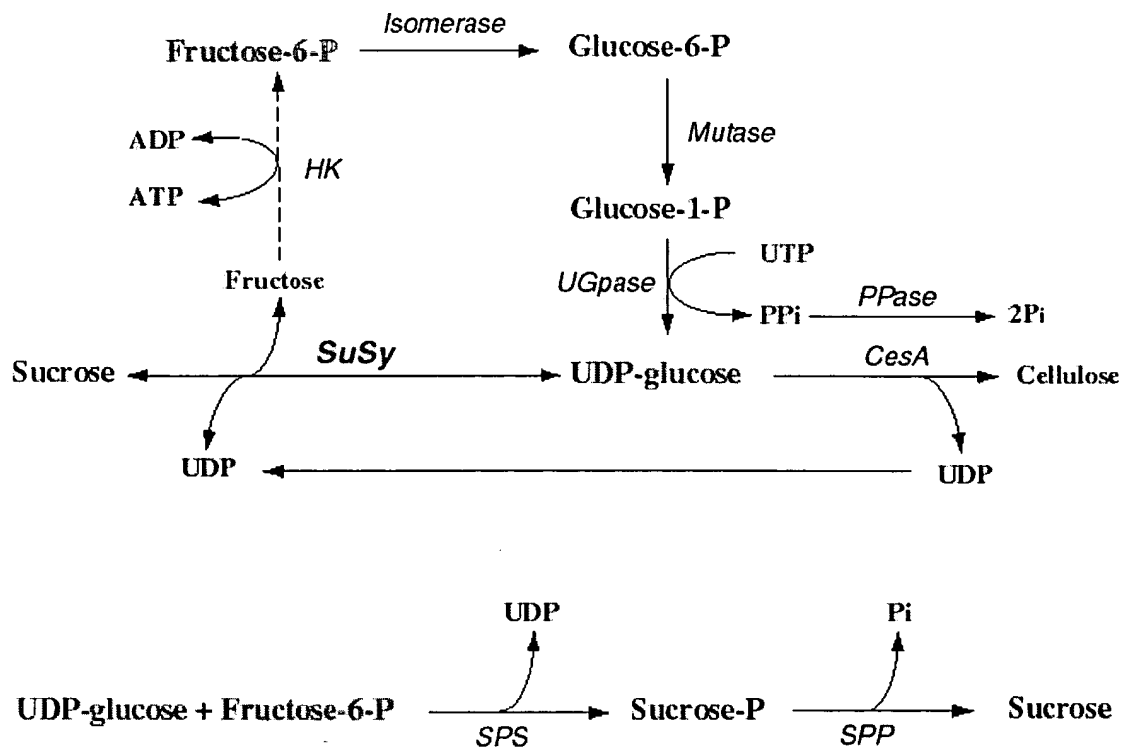
Figure 3.
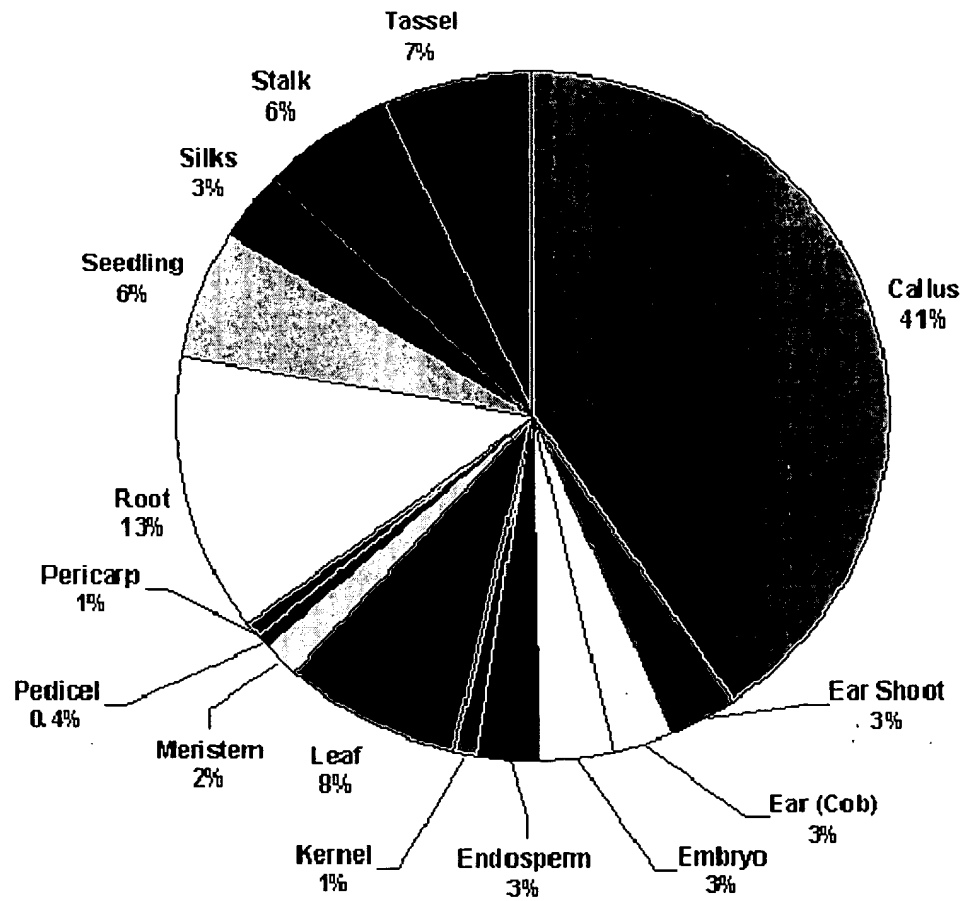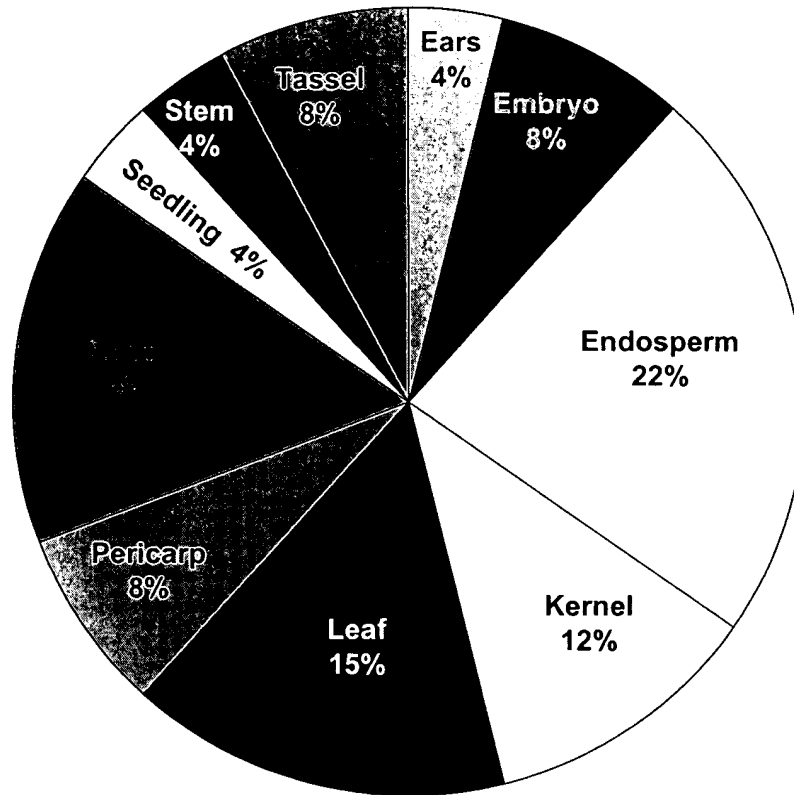
Figure 4.

Figure 5

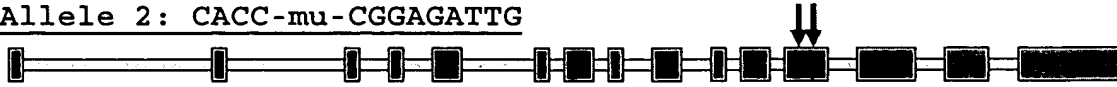Allele 1: CACCCGG-mu-AGATTG

Allele 2: CACC-mu-CGGAGATTG

Figure 6.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
Sus-1 (WT)	63.2	25.2 +/-0.38	39.9
sus-1 (mutant)	47.3	17.7 +/-0.34	37.4

Figure 7.

```
                  1                                                50
Sh1         (1)   -----MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVHQGKGMLQRHQ
Sus1        (1)   MGEGAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLGKGMLQPHQ
Sus3        (1)   ----------STHASGDRVEDTLHAHRNELVALLSKYVNKGKGILQPHH
Consensus   (1)        LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLQPHQ

                  51                                               100
Sh1        (46)   LLAEFD-ALFDSDKE--KYAPFEDILRAAQEAIVLPPWVALAIRPRPGVW
Sus1       (51)   ITAEYNNAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVW
Sus3       (40)   ILDALDEVQGSGGRA-LAEGPFLDVLRSAQEAIVLPPFVAIAVRPRPGVW
Consensus  (51)   ILAEFD AI DADRE LKDGPFEDVLRAAQEAIVLPPWVALAIRPRPGVW

                  101                                              150
Sh1        (93)   DYIRVNVSELAVEELSVSEYLAFKEQLVDGQSNSNFVLELDFEPFNASFP
Sus1      (101)   EYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNFVLELDFEPFNASFP
Sus3       (89)   EYVRVNVHELSVEQLTVSEYLRFKEELVDGQHNDPYVLELDFEPFNVSVP
Consensus (101)   EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLELDFEPFNASFP

                  151                                              200
Sh1       (143)   RPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNYKGTTMMLN
Sus1      (151)   RPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLN
Sus3      (139)   RPNRSSSIGNGVQFLNRHLSSIMFRNRDCLEPLLDFLRGHRHKGHVMMLN
Consensus (151)   RPSLSKSIGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNYKG TMMLN

                  201                                              250
Sh1       (193)   DRIQSLRGLQSSLRKAEEYLLSVPQDTPYSEFNHRFQELGLEKGWGDTAK
Sus1      (201)   DRIRSLSALQGALRKAEEHLSTLQADTPYSEFHHRFQELGLEKGWGDCAK
Sus3      (189)   DRIQSLGRLQSVLTKAEEHLSKLPADTPYSQFAYKFQEWGLEKGWGDTAG
Consensus (201)   DRIQSL ALQSALRKAEEHLSSLPADTPYSEF HRFQELGLEKGWGDTAK

                  251                                              300
Sh1       (243)   RVLDTLHLLLDLLEAPDPANLEKFLGTIPMMFNVVILSPHGYFAQSNVLG
Sus1      (251)   RAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLG
Sus3      (239)   HVLEMIHLLLDIIQAPDPSTLEKFLGRIPMIFNVVVSPHGYFGQANVLG
Consensus (251)   RVLETIHLLLDLLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG

                  301                                              350
Sh1       (293)   YPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAAGT
Sus1      (301)   YPDTGGQVVYILDQVRAMENEMLLRIKQCGLDITPKILIVTRLLPDATGT
Sus3      (289)   LPDTGGQIVYILDQVRALENEMVLRLKKQGLDVSPKILIVTRLIPDAKGT
Consensus (301)   YPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDA GT

                  351                                              400
Sh1       (343)   TCGQRLEKVIGTEHTDIIRVPFRNENGILRKWISRFDVWPYLETYTEDVS
Sus1      (351)   TCGQRLEKVLGTEHCHILRVPFRTENGIVRKWISRFEVWPYLETYTDDVA
Sus3      (339)   SCNQRLERISGTQHTYILRVPFRNENGILKKWISRFDVWPYLETFAEDAA
Consensus (351)   TCGQRLEKVIGTEHTHILRVPFRNENGILRKWISRFDVWPYLETYTEDVA

                  401                                              450
Sh1       (393)   SEIMKEMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPN
Sus1      (401)   HEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPN
Sus3      (389)   GEIAAELQGTPDFIIGNYSDGNLVASLLSYKMGITQCNIAHALEKTKYPD
Consensus (401)    EIAAELQA PDLIIGNYSDGNLVASLLAHKMGVTQCTIAHALEKTKYPN

                  451                                              500
Sh1       (443)   SDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYE
Sus1      (451)   SDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYE
Sus3      (439)   SDIFWKNFDEKYHFSCQFTADIIAMNNADFIITSTYQEIAGSKNTVGQYE
Consensus (451)   SDIYWKKFDD YHFSCQFTADLIAMNHADFIITSTFQEIAGSKDTVGQYE

                  501                                              550
Sh1       (493)   SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYYPYTETDKRLTAFH
Sus1      (501)   SHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLH
Sus3      (489)   SHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPHTEKAKRLTSLH
Consensus (501)   SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTES KRLTSLH
```

Figure 8a

```
          551                                              600
Sh1       (543) PEIEELIYSDVENSEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGKN
Sus1      (551) PEIEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRN
Sus3      (539) GSIENLIYDPEQNDEHIGHLDDRSKPILFSMARLDRVKNITGLVEAFAKC
Consensus (551) PEIEELIYS  ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN
          601                                              650
Sh1       (593) ARLRELANLVIVAGDHGK-ESKDREEQAEFKKMYSLIDEYKLKGHIRWIS
Sus1      (601) KRLQELVNLVVVCGDHGN-PSKDKEEQAEFKKMFDLIEQYNLNGHIRWIS
Sus3      (589) AKLRELVNLVVVAGYNDVNKSKDREEIAEIEKMHELIKTHNLFGQFRWIS
Consensus (601) ARLRELVNLVVVAGDHG   SKDREEQAEFKKMHDLID YNL GHIRWIS
          651                                              700
Sh1       (642) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVIESMTCGLPTIATCH
Sus1      (650) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATAY
Sus3      (639) AQTNRARNGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLH
Consensus (651) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFAT H
          701                                              750
Sh1       (692) GGPAEIIVDGVSGLHIDPYHSDKAADILVNFFDKCKADPSYWDEISQGGL
Sus1      (700) GGPAEIIVHGVSGYHIDPYQGDKASALLVDFFDKCQAEPSHWSKISQGGL
Sus3      (689) GGPAEIIEHGVSGFHIDPYHPEQAVNLMADFFDRCKQDPDHWVNISGAGL
Consensus (701) GGPAEIIVHGVSGFHIDPYH DKAA LLVDFFDKCKADPSHW  ISQGGL
          751                                              800
Sh1       (742) QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYIEMFYALKYR
Sus1      (750) QRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYR
Sus3      (739) QRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERLETRRYLEMFYILKFR
Consensus (751) QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR
          801            817
Sh1       (792) SLASQVPLSFD------
Sus1      (800) TMASTVPLAVEGEPSSK
Sus3      (789) ELAKTVPLAID-QPQ--
Consensus (801) SLASTVPLAID  P
```

Figure 8b

```
                        1                                           50
Sh1         (1)  AAACCCTCCCTCCCTCCTCCATTGGACTGCTTGCTCCCTGTTGACCATTG
Sus1        (1)  ----------------------GCCTGAG-GATCCAGGAAGAGGACAG
Sus3        (1)  --------------------------------------------------
Consensus   (1)                        G CTG    G TCC  G  GA  A  G
                        51                                          100
Sh1        (51)  GGTATTCTGAACCATCGAGCCATGGCTGCCAAGCTGACTCGCCTTCACAG
Sus1       (26)  CA-ATGGGGGAAGGTGCAGGTGACCGTGTC---CTGAGCCGCCTCCACAG
Sus3        (1)  ---------------------------------------GTCGAC-CCACGC
Consensus  (51)       AT   G A   T  AG       TG C   CTGAGTCGCCTCCACAG
                        101                                         150
Sh1       (101)  TCTTCGCGAACGCCTTGGTGCCACCTTCTCCTCCCATCCCAATGAACTGA
Sus1       (72)  CGTCAGGGAGCGCATTGGCGACTCACTCTCTGCCCACCCCAATGAGCTTG
Sus3       (13)  GTCCGGCGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGCTCG
Consensus (101)     TC GCGA CGC TTGG  GACACCCTCTCCGCCCACCCCAATGAGCT G
                        151                                         200
Sh1       (151)  TAGCACTCTTTTCCAGGTATGTTCACCAGGGCAAGGGAATGCTTCAGCGC
Sus1      (122)  TCGCCGTCTTCACCAGGCTGAAAAACCTTGGAAAGGGTATGCTGCAGCCC
Sus3       (63)  TCGCCCTCCTGTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCG
Consensus (151)  TCGCCCTCTT  TCCAGGTA GT AACCAGGG AAGGG ATGCTGCAGCCC
                        201                                         250
Sh1       (201)  CATCAGCTGCTTGCGGAGTTTGA---TGC----CCTGTT--TGATAGTGA
Sus1      (172)  CACCAGATCATTGCCGAGTACAACAATGCGATCCCTGAGGCTGAGCGCGA
Sus3      (113)  CACCACATCCTCGACGCGCTCGACGAGGT----CCAGGG-CTCCGGGGGC
Consensus (201)  CACCAGATCCTTGCCGAGTTCGAC ATGC     CCTG G CTGAG G GA
                        251                                         300
Sh1       (242)  CAAGGAGAAG--TATGCACCATTTGAAGACATTCTTCGTGCTGCTCAGGA
Sus1      (222)  GAAGCTCAAG--GATGGTGCTTTTGAGGATGTCCTGAGGGCAGCTCAGGA
Sus3      (158)  CGCGCGCTAGCCGAGGGACCCTTCCTCGACGTCCTCCGCTCCGCGCAGGA
Consensus (251)  CAAGC CAAG   GATGGACC TTTGA GACGTCCT CG GC GCTCAGGA
                        301                                         350
Sh1       (290)  AGCAATTGTGCTCCCCCCATGGGTTGCACTTGCTATCAGGCCAAGGCCTG
Sus1      (270)  GGCGATTGTCATCCCCCCATGGGTTGCACTTGCCATCCGCCCTAGGCCTG
Sus3      (208)  GGCGATCGTGCTGCCGCCGTTCGTGGCCATCGCGGTGCGCCCGCGCCCGG
Consensus (301)  GGCGATTGTGCTCCCCCCATGGGTTGCACTTGC ATCCGCCC AGGCCTG
                        351                                         400
Sh1       (340)  GTGTCTGGGATTACATTCGGGTGAATGTAAGTGAGCTGGCTGTGGAGGAG
Sus1      (320)  GTGTCTGGGAGTATGTGAGGGTCAACGTCAGTGAGCTCGCTGTTGAGGAG
Sus3      (258)  GAGTTTGGGAGTACGTCCGCGTCAACGTTCACGAGCTCAGCGTCGAGCAG
Consensus (351)  GTGTCTGGGAGTACGT CGGGTCAACGT AGTGAGCTCGCTGT GAGGAG
                        401                                         450
Sh1       (390)  CTGAGTGTTTCTGAGTACTTGGCATTCAAGGAACAGCTGGTGGATGGACA
Sus1      (370)  CTGAGAGTTCCTGAGTACCTGCAGTTCAAGGAACAGCTTGTGGAAGAAGG
Sus3      (308)  CTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTTGTCGACGGCCA
Consensus (401)  CTGAGAGTTTCTGAGTACCTGC  TTCAAGGAACAGCTTGTGGA GGACA
                        451                                         500
Sh1       (440)  ATCCAACAGCAACTTTGTGCTTGAGCTTGATTTTGAGCCCTTCAATGCCT
Sus1      (420)  CCCCAACAACAACTTTGTTCTTGAGCTGGACTTTGAGCCATTCAATGCCT
Sus3      (358)  GCACAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCCGTTCAATGTCT
Consensus (451)   CCCAACAACAACTTTGTTCTTGAGCTTGACTTTGAGCC TTCAATGCCT
                        501                                         550
Sh1       (490)  CCTTTCCTCGTCCTTCCATGTCGAAGTCCATCGGAAATGGAGTGCAATTC
Sus1      (470)  CCTTCCCCCGTCCTTCTCTGTCAAAGTCCATTGGCAATGGCGTGCAGTTC
Sus3      (408)  CAGTCCCACGCCCAAATCGGTCATCATCTATTGGAAACGGTGTGCAGTTC
Consensus (501)  CCTTCCC CGTCCTTCTCTGTCAAAGTCCATTGGAAATGG GTGCAGTTC
```

Figure 9a

```
                      551                                        600
      Sh1    (540)  CTTAACCGACACCTGTCGTCCAAGTTGTTCCAGGACAAGGAGAGTTTGTA
      Sus1   (520)  CTCAACAGGCACCTGTCATCAAAGCTCTTCCATGACAAGGAGAGCATGTA
      Sus3   (458)  CTCAACCGACACTTGTCCTCAATCATGTTCCGCAACAGGGATTGCTTGGA
 Consensus   (551)  CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGTA
                      601                                        650
      Sh1    (590)  CCCCTTGCTGAACTTCCTCAAGGCTCATAACTACAAGGGCACGACGATGA
      Sus1   (570)  CCCCTTGCTCAACTTCCTTCGCGCCCACAACTACAAGGGGATGACCATGA
      Sus3   (508)  GCCCCTGTTGGATTTCCTCCGTGGCCACCGGCACAAGGGGCATGTTATGA
 Consensus   (601)  CCCCTTGCTGAACTTCCTCCG GCCCACAACTACAAGGGGA GAC ATGA
                      651                                        700
      Sh1    (640)  TGTTGAATGACAGAATCCAAAGCCTTCGTGGTCTCCAATCATCCCTGAGA
      Sus1   (620)  TGTTGAACGACAGAATCCGCAGTCTCAGTGCTCTGCAAGGTGCGCTGAGG
      Sus3   (558)  TGCTTAATGATAGAATACAAAGCTTGGGGAGGCTTCAGTCTGTGCTGACC
 Consensus   (651)  TGTTGAATGACAGAATCCAAAGCCT  GTGGTCT CAATCTGCGCTGAG
                      701                                        750
      Sh1    (690)  AAGGCAGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA
      Sus1   (670)  AAGGCTGAGGAGCACCTGTCCACCCTACAAGCTGATACCCCATACTCTGA
      Sus3   (608)  AAAGCTGAGGAGCACTTGTCAAAGCTCCCTGCTGACACACCATACTCACA
 Consensus   (701)  AAGGCTGAGGAGCACCTGTC A  CT CCTGCTGACAC CCATACTC GA
                      751                                        800
      Sh1    (740)  GTTCAACCATAGGTTCCAAGAGCTTGGCTTGGAGAAGGGTTGGGGTGACA
      Sus1   (720)  ATTTCACCACAGGTTCCAGGAACTTGGTCTGGAGAAGGGTTGGGGTGATT
      Sus3   (658)  ATTTGCTTATAAATTTCAAGAGTGGGGCCTGGAGAAAGGTTGGGGTGATA
 Consensus   (751)  ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGGTTGGGGTGATA
                      801                                        850
      Sh1    (790)  CTGCGAAGCGTGTTCTCGACACACTCCACTTGCTTCTCGACCTTCTTGAG
      Sus1   (770)  GCGCTAAGCGTGCACAGGAGACTATCCACCTCCTCTTGGACCTCCTGGAG
      Sus3   (708)  CAGCAGGACATGTTTTGGAAATGATCCATCTCCTTCTAGACATCATTCAG
 Consensus   (801)  C GC AAGCGTGTTCTGGA AC ATCCACCTCCTTCT GACCTCCTTGAG
                      851                                        900
      Sh1    (840)  GCCCCTGATCCTGCCAACTTGGAGAAGTTCCTTGGAACTATACCAATGAT
      Sus1   (820)  GCCCCAGATCCGTCCACCCTGGAGAAGTTCCTTGGAACGATCCCCATGGT
      Sus3   (758)  GCGCCAGACCCATCTACCCTAGAGAAATTCTTGGGGAGGATCCCCATGAT
 Consensus   (851)  GCCCCAGATCC TCCACCCTGGAGAAGTTCCTTGGAACGATCCCCATGAT
                      901                                        950
      Sh1    (890)  GTTCAACGTTGTTATCCTGTCTCCTCATGGCTACTTCGCCCAGTCCAATG
      Sus1   (870)  GTTCAATGTCGTTATCCTCTCCCCTCATGGTTACTTCGCTCAAGCTAATG
      Sus3   (808)  TTTTAACGTTGTTGTGGTATCCCCTCATGGATACTTTGGTCAAGCTAATG
 Consensus   (901)  GTTCAACGTTGTTATCCT TCCCCTCATGG TACTTCGCTCAAGCTAATG
                      951                                        1000
      Sh1    (940)  TGCTTGGATACCTGACACTGGCGGTCAGGTTGTGTACATTCTGGATCAA
      Sus1   (920)  TCTTGGGTTACCCTGACACCGGAGGCCAGGTTGTCTACATCTTGGATCAA
      Sus3   (858)  TATTAGGCTTGCCAGACACAGGAGGACAGATCGTCTATATACTGGACCAA
 Consensus   (951)  T TT GG TACCCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA
                      1001                                       1050
      Sh1    (990)  GTCCGTGCTTTGGAGAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCCT
      Sus1   (970)  GTGCGCGCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGGTCT
      Sus3   (908)  GTCCGTGCACTAGAAAATGAGATGGTTCTCCGTTTAAAGAAACAAGGGCT
 Consensus   (1001) GTCCGTGCT TGGAGAATGAGATGCTTCTGAGGAT AAGCAGCAAGG CT
```

Figure 9b

```
                    1051                                                1100
       Sh1   (1040) TGATATCACTCCGAAGATCCTCATTGTTACCAGGCTGTTGCCTGATGCTG
       Sus1  (1020) TGACATCACGCCGAAGATCCTTATTGTCACCAGGTTGCTCCCTGATGCAA
       Sus3   (958) TGATGTTTCCCCAAAGATTCTCATTGTTACTCGGCTGATACCAGATGCAA
  Consensus  (1051) TGATATCAC CCGAAGATCCTCATTGTTACCAGGCTG T CCTGATGCAA

                    1101                                                1150
       Sh1   (1090) CTGGGACTACGTGCGGTCAGCGGCTGGAGAAGGTCATTGGTACTGAGCAC
       Sus1  (1070) CTGGCACCACCTGTGGCCAGCGCCTTGAGAAGGTCCTTGGCACCGAGCAC
       Sus3  (1008) AAGGAACATCATGCAATCAGCGGCTTGAGAGAATTAGTGGAACACAGCAT
  Consensus  (1101) CTGG AC AC TGCGGTCAGCGGCTTGAGAAGGTCATTGG AC GAGCAC

                    1151                                                1200
       Sh1   (1140) ACAGACATCATTCGCGTTCCCTTCAGAAATGAGAATGGCATCCTCCGCAA
       Sus1  (1120) TGCCATATCCTTCGCGTGCCATTCAGAACAGAAAACGGAATCGTTCGCAA
       Sus3  (1058) ACTTACATATTACGAGTTCCCTTCAGAAATGAAAATGGGATACTTAAGAA
  Consensus  (1151) AC   ACATC TTCGCGTTCCCTTCAGAAATGAAAATGG ATCCTTCGCAA

                    1201                                                1250
       Sh1   (1190) GTGGATCTCTCGTTTTGATGTCTGGCCATACCTGGAGACATACACTGAGG
       Sus1  (1170) GTGGATCTCGCGATTTGAAGTCTGGCCGTACCTGGAGACTTACACTGATG
       Sus3  (1108) ATGGATATCAAGATTTGATGTGTGGCCATATCTGGAAACATTTGCTGAGG
  Consensus  (1201) GTGGATCTC CGATTTGATGTCTGGCCATACCTGGAGACATACACTGAGG

                    1251                                                1300
       Sh1   (1240) ATGTTTCCAGTGAAATAATGAAAGAAATGCAGGCCAAGCCTGACCTTATC
       Sus1  (1220) ACGTGGCGCATGAGATTGCTGGAGAGCTTCAGGCCAATCCTGACCTGATC
       Sus3  (1158) ATGCTGCTGGTGAAATTGCTGCTGAATTACAAGGTACTCCAGACTTCATA
  Consensus  (1251) ATGTTGC  GTGAAATTGCTG AGAA T CAGGCCAATCCTGACCT ATC

                    1301                                                1350
       Sh1   (1290) ATTGGCAACTACAGCGATGGCAACCTAGTCGCCACTCTGCTCGCGCACAA
       Sus1  (1270) ATCGGAAACTACAGTGACGGAAACCTTGTTGCGTGTTTGCTCGCCCACAA
       Sus3  (1208) ATTGGAAACTACAGTGATGGAAATCTTGTGGCGTCATTGCTATCTTACAA
  Consensus  (1301) ATTGGAAACTACAGTGATGGAAACCTTGT GCGTCTTTGCTCGC CACAA

                    1351                                                1400
       Sh1   (1340) GTTGGGAGTCACTCAGTGTACCATCGCTCATGCCTTGGAGAAAACCAAAT
       Sus1  (1320) GATGGGTGTTACTCACTGTACCATTGCCCATGCGCTTGAGAAAACTAAGT
       Sus3  (1258) GATGGGAATTACCAGTGCAACATTGCTCATGCTCTGGAAAAGACTAAGT
  Consensus  (1351) GATGGGAGTTACTCAGTGTACCATTGCTCATGC CTGGAGAAAACTAAGT

                    1401                                                1450
       Sh1   (1390) ACCCCAACTCGGACATCTACTTGGACAAATTCGACAGCCAGTACCACTTC
       Sus1  (1370) ACCCTAACTCCGACCTCTACTGGAAGAAGTTTGAGGATCACTACCACTTC
       Sus3  (1308) ATCCAGATTCAGACATATTTTGGAAGAATTTCGATGAGAGTACCATTTC
  Consensus  (1401) ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC

                    1451                                                1500
       Sh1   (1440) TCTTGCCAGTTCACAGCTGACCTTATTGCCATGAACCACACCGATTTCAT
       Sus1  (1420) TCGTGCCAGTTCACCACTGACTTGATTGCAATGAACCATGCCGACTTCAT
       Sus3  (1358) TCCTGCCAGTTCACTGCTGATATAATTGCTATGAACAATGCTGATTTTAT
  Consensus  (1451) TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTCAT

                    1501                                                1550
       Sh1   (1490) CATCACCAGCACATTCCAAGAAATCGCGGGAAGCAAGGACACCGTGGGGC
       Sus1  (1470) CATCACCAGTACCTTCCAAGAGATCGCCGGAAACAAGGACACCGTCGGCC
       Sus3  (1408) CATCACCAGCACATACCAAGAAATTGCTGGAAGCAAAAATACTGTTGGAC
  Consensus  (1501) CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C
```

Figure 9c

```
                       1551                                              1600
        Sh1    (1540)  AGTACGAGTCCCATATCGCGTTCACTCTTCCTGGGCTCTACCGTGTCGTC
        Sus1   (1520)  AGTACGAGTCACACATGGCGTTCACAATGCCTGGCCTGTACCGCGTTGTC
        Sus3   (1458)  AGTATGAGAGTCATACTGCCTTTACTCTGCCTGGTCTGTACCGAGTTGTC
   Consensus   (1551)  AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC
                       1601                                              1650
        Sh1    (1590)  CATGGCATCGATGTTTTCGATCCCAAGTTCAACATTGTCTCTCCTGGAGC
        Sus1   (1570)  CACGGCATTGATGTGTTCGACCCCAAGTTCAACATCGTGTCTCCTGGCGC
        Sus3   (1508)  CATGGGATCGATGTCTTCGATCCAAAGTTCAATATAGTCTCTCCTGGAGC
   Consensus   (1601)  CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCCTGGAGC
                       1651                                              1700
        Sh1    (1640)  AGACATGAGTGTTTACTACCCTTATACGGAAACCGACAAGAGACTCACTG
        Sus1   (1620)  GGACCTGTCCATCTACTTCCCGTACACCGAGTCGCACAAGAGGCTGACCT
        Sus3   (1558)  TGACATGTCCATATACTTTCCACATACCGAGAAGGCCAAGCGACTCACCT
   Consensus   (1651)   GACATGTCCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT
                       1701                                              1750
        Sh1    (1690)  CCTTCCATCCTGAAATCGAGGAGCTCATCTACAGCGACGTCGAGAACTCC
        Sus1   (1670)  CCCTTCACCCGGAGATTGAGGAGCTCCTGTACAGCCAAACCGAGAACACG
        Sus3   (1608)  CTCTTCATGGTTCAATCGAAAATTTGATTTATGACCCGGAGCAAAACGAT
   Consensus   (1701)  CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C
                       1751                                              1800
        Sh1    (1740)  GAGCACAAGTTCGTGCTGAAGGACAAGAAGAAGCCGATCATCTTCTCGAT
        Sus1   (1720)  GAGCACAAGTTCGTTCTGAACGACAGGAACAAGCCAATCATCTTCTCCAT
        Sus3   (1658)  GAACACATTGGGCATCTGGATGACCGGTCAAAGCCCATCCTCTTCTCCAT
   Consensus   (1751)  GAGCACAAGTTCGTTCTGAA GACAGGAA AAGCC ATCATCTTCTCCAT
                       1801                                              1850
        Sh1    (1790)  GGCGCGTCTCGACCGCGTGAAGAACATGACAGGCCTGGTCGAGATGTACG
        Sus1   (1770)  GGCTCGTCTCGACCGTGTGAAGAACTTGACTGGGCTGGTGGAGCTGTACG
        Sus3   (1708)  GGCAAGACTCGACAGGGTGAAGAACATAACAGGGCTGGTCGAAGCTTTTG
   Consensus   (1801)  GGC CGTCTCGACCG GTGAAGAACATGACAGGGCTGGTCGAG TGTACG
                       1851                                              1900
        Sh1    (1840)  GCAAGAACGCGCGCCTGAGGGAGCTGGCGAACCTCGTGATCGTTGCCGGT
        Sus1   (1820)  GCCGGAACAAGCGGCTGCAGGAGCTGGTGAACCTCGTGGTCGTCTGCGGC
        Sus3   (1758)  CTAAGTGCGCTAAGCTGAGGGAGCTGGTAAACCTTGTCGTCGTTGCCGGG
   Consensus   (1851)  GCAAGAACGCGCGGCTGAGGGAGCTGGTGAACCTCGTGGTCGTTGCCGG
                       1901                                              1950
        Sh1    (1890)  GACCACGG---CAAGGAGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA
        Sus1   (1870)  GACCATGG---CAACCCTTCCAAGGACAAGGAGGAGCAGGCCGAGTTCAA
        Sus3   (1808)  TACAATGATGTCAACAAGTCCAAGGACAGGGAAGAGATCGCGGAGATAGA
   Consensus   (1901)  GACCATGG    CAAC AGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA
                       1951                                              2000
        Sh1    (1937)  GAAGATGTACAGCCTCATCGACGAGTACAAGTTGAAGGGCCATATCCGGT
        Sus1   (1917)  GAAGATGTTTGACCTCATCGAGCAGTACAACCTGAACGGGCACATCCGCT
        Sus3   (1858)  GAAGATGCATGAACTCATCAAGACCCACAACTTGTTCGGGCAGTTCCGCT
   Consensus   (1951)  GAAGATGTATGACCTCATCGAG AGTACAACTTGAACGGGCA ATCCGCT
                       2001                                              2050
        Sh1    (1987)  GGATCTCGGCGCAGATGAACCGTGTCCGCAACGGGGAGCTGTACCGCTAC
        Sus1   (1967)  GGATCTCCGCCCAGATGAACCGCGTCCGCAACGGCGAGCTGTACCGCTAC
        Sus3   (1908)  GGATCTCTGCCCAGACAAACAGGGCCCGTAACGGCGAGCTCTATCGCTAC
   Consensus   (2001)  GGATCTC GCCCAGATGAACCG GTCCGCAACGGCGAGCTGTACCGCTAC
                       2051                                              2100
        Sh1    (2037)  ATTTGCGATACCAAGGGCGCATTCGTGCAGCCTGCGTTCTACGAAGCGTT
        Sus1   (2017)  ATCTGCGACACCAAGGGCGCCTTCGTGCAGCCTGCTTTCTACGAGGCTTT
        Sus3   (1958)  ATCGCTGATACCCATGGTGCTTTCGTACAGCCGGCCTTGTATGAAGCGTT
   Consensus   (2051)  ATCTGCGATACCAAGGGCGC TTCGTGCAGCCTGC TTCTACGAAGCGTT
```

Figure 9d

```
                        2101                                              2150
      Sh1    (2087)  CGGCCTGACTGTGATCGAGTCCATGACGTGCGGTCTGCCAACGATCGCGA
      Sus1   (2067)  CGGGCTGACGGTGGTTGAGGCCATGACCTGCGGCCTGCCCACGTTCGCCA
      Sus3   (2008)  CGGTCTCACCGTCGTTGAGGCCATGACCTGTGGGCTTCCTACTTTCGCGA
  Consensus  (2101)  CGG CTGAC GTGGTTGAGGCCATGACCTGCGG CTGCC ACGTTCGCGA
                        2151                                              2200
      Sh1    (2137)  CCTGCCATGGCGGCCCTGCTGAGATCATCGTGGACGGGGTATCTGGCCTG
      Sus1   (2117)  CCGCCTACGGCGGTCCGGCCGAGATCATCGTGCACGGCGTGTCTGGCTAC
      Sus3   (2058)  CGCTCCATGGAGGTCCAGCTGAGATCATAGAGCATGGCGTCTCGGGCTTC
  Consensus  (2151)  CC  CCATGGCGGTCC GCTGAGATCATCGTGCACGGCGT TCTGGCTTC
                        2201                                              2250
      Sh1    (2187)  CACATTGACCCTTACCACAGCGACAAGGCCGCGGATATCCTGGTCAACTT
      Sus1   (2167)  CACATCGACCCTTACCAGGGCGACAAGGCGTCGGCCCTGCTCGTGGACTT
      Sus3   (2108)  CACATTGACCCGTACCACCCCGAACAGGCTGTTAATCTGATGGCCGACTT
  Consensus  (2201)  CACATTGACCCTTACCAC GCGACAAGGC GCGGATCTGCTGGTCGACTT
                        2251                                              2300
      Sh1    (2237)  CTTTGACAAATGCAAGGCAGATCCGAGCTACTGGGACGAGATCTCACAGG
      Sus1   (2217)  CTTCGACAAGTGCCAGGCGGAGCCGAGCCACTGGAGCAAGATCTCCCAGG
      Sus3   (2158)  CTTCGACCGGTGCAAGCAAGACCCAGATCACTGGGTGAATATATCTGGAG
  Consensus  (2251)  CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG
                        2301                                              2350
      Sh1    (2287)  GCGGCCTGCAGAGAATTTATGAGAAGTACACCTGGAAGCTCTACTCCGAG
      Sus1   (2267)  GCGGGCTCCAGCGTATCGAGGAGAAGTACACCTGGAAGCTGTACTCGGAG
      Sus3   (2208)  CAGGGCTGCAGCGCATATACGAGAAGTACACATGGAAGATATACTCAGAG
  Consensus  (2301)  GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG
                        2351                                              2400
      Sh1    (2337)  AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGAGCAA
      Sus1   (2317)  AGGCTGATGACCCTCACCGGCGTGTACGGGTTCTGGAAGTACGTGTCCAA
      Sus3   (2258)  AGGTTGATGACACTGGCCGGGGTCTACGGTTTCTGGAAGTACGTGTCGAA
  Consensus  (2351)  AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGTCCAA
                        2401                                              2450
      Sh1    (2387)  CCTGGAGAGGCGCGAGACCCGCCGCTACATCGAGATGTTCTACGCCCTGA
      Sus1   (2367)  CCTGGAGAGGCGCGAGACCCGGCGGTACCTGGAGATGCTGTACGCGCTCA
      Sus3   (2308)  GCTCGAGAGGCTGGAGACGAGGCGCTACCTTGAGATGTTCTACATACTGA
  Consensus  (2401)  CCTGGAGAGGCGCGAGACCCGGCGCTACCT GAGATGTTCTACGC CTGA
                        2451                                              2500
      Sh1    (2437)  AGTACCGTAGCCTGGCAAGCCAGGTTCCGCTGTCCTTCGA------TTAG
      Sus1   (2417)  AGTACCGCACCATGGCGAGCACCGTGCCGCTGGCCGTGGA------GGGA
      Sus3   (2358)  AGTTCCGCGAGCTGGCGAAGACCGTGCCGCTTGCAATTGACCAACCGCAG
  Consensus  (2451)  AGTACCGCA CCTGGCGAGCACCGTGCCGCTGGCC T GA    G AG
                        2501                                              2550
      Sh1    (2481)  TACGGGGAAAGAAGGAGA-AGAAGAAGAAGAAGCCCAGGCCGGA-----G
      Sus1   (2461)  GAGCCCTCCAGCAAGTGA-TGCGTGACGGCGGCCACAGACCTGATC---G
      Sus3   (2408)  TAGCTTGCGCAACTGCGACTGCGTAGCACTTGGTACAAGACTGAAACCTG
  Consensus  (2501)  TAGC  GC AGAA G GA TGCGTAACA   GGCACAGGCCTGA      G
                        2551                                              2600
      Sh1    (2525)  AACCATCGCCTGCATTTCGATCT--------GT-TTCACCGCAATTCGC
      Sus1   (2507)  ATCGATGAGCGAGAGGGAGCACTCGGA-----GT-GTCGTGTCTTTTCCC
      Sus3   (2458)  AAGGACCTTCAGTAATTTAGGCGCGGCAGACGGTAGCCAATAAAATGTGC
  Consensus  (2551)  AACGATC  C G A TT G CTCGG        GT GTCA   CAATTCGC
```

Figure 9e

```
                  2601                                              2650
       Sh1   (2565) ATTGTTAGTCGTGTATTGGAGTTATGTG--TACTTGGTTTCCAAGAACTT
       Sus1  (2551) TTGCCATTTCTTTCTTTCTTCTTTTTCC--TTCCCGGAGGCGAAAAAAA
       Sus3  (2508) CGGAGCTGAACTGGTTTTTTATTATGTACATAATGGCAGTATAACAAAAT
  Consensus  (2601) TG     TGTC TG TTT TT TTATGT   TACT GGAGTC AA AAAAT
                  2651                                              2700
       Sh1   (2613) TGGTTCCTTCTCGTTTTTTTTCCTTGTTTGAGCGTTTTTGGGCAGCGCTG
       Sus1  (2599) AGAGTC-TGCTT-TTGCTAGGCGGCGGGCGTTCGTTGCTGCTCTTTGCTT
       Sus3  (2558) TACTGAAGGCAGGTGGGTTGCAGTTGTGTGTTCGTTACTG-------TT
  Consensus  (2651) TG TTC TGCT GTTG TTG CGTTGTGTGTTCGTT CTG   C   GCT
                  2701                                              2750
       Sh1   (2663) GCCTGGTTCCTAGTATGGTGGGAATTGGCTGCACCTTTTGCTTCGAATAA
       Sus1  (2647) CAAGAGTTAAAATTTACCTACC--TTGTCAAGGTCTTGTTCCATCATTGA
       Sus3  (2600) TACTGTATTATGTCAAGCTGTC----GGCTGCAATTTCTTTGCTGG--CA
  Consensus  (2701)  ACTGGTT ATATTAAGCTG C   TTGGCTGCA CTT TTC   TGA T A
                  2751                                              2800
       Sh1   (2713) AAATGCCTGCTCGTTCACCTGTCTTCCAGAGTGC----------------
       Sus1  (2695) TCCGGGTGTCGCTTGTAGTAGTCTGATGGACTGTTAGTAGTTTGCGTTGC
       Sus3  (2644) AGCCGCAGGCACTGGTGAAGTGCTGATAAATACATCATATTCTGTTGACC
  Consensus  (2751) A C GC GGC CTTGTA    GTCTGATAGA TG T  TA T TG      C
                  2801                                              2850
       Sh1   (2747) --------------------------------------------------
       Sus1  (2745) GTCGGTTGAGAGGGAACGTTGGTGGTGGTGGTGTGTGTGCAGTCAGGCGT
       Sus3  (2694) TGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC------
  Consensus  (2801)    G    A A   AA                   G  G  G     C

                  2851                                              2900
       Sh1   (2747) --------------------------------------------------
       Sus1  (2795) GGTGCTCCCTTTGTTTCCTGGATGGGATGTTGCTCCTTGAATAATAATCG
       Sus3  (2738) --------------------------------------------------
  Consensus  (2851)
                  2901                                              2950
       Sh1   (2747) --------------------------------------------------
       Sus1  (2845) TAGTGGCCTTGGAGCCCTTTTCCTGAAATAAGAGCAGCATCCTAGTGCTT
       Sus3  (2738) --------------------------------------------------
  Consensus  (2901)
                  2951       2964
       Sh1   (2747) --------------
       Sus1  (2895) ACCTTTGCAGCTGT
       Sus3  (2738) --------------
  Consensus  (2951)
```

Figure 9f

CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG

CGCGCGCGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCC<u>ATGTCTGCCCCGAAGCTGA</u>

<u>ACCGCAACGCGAGCATCCGGG</u>ACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC

TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA

TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT

TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

Figure 10

Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11
ATGTCTGCCCCGAAGCTGAACCGCAACGCGAGCATCCGG

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

```
gtcgacccac gcgtccggcg accgcgtcga ggacaccctc cacgcgcacc gcaacgagct      60
cgtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atcctgcagc cgcaccacat     120
cctcgacgcg ctcgacgagg tccagggctc cggggggccgc gcgctagccg agggaccctt     180
cctcgacgtc ctccgctccg cgcaggaggc gatcgtgctg ccgccgttcg tggccatcgc     240
ggtgcgcccg cgcccgggag tttgggagta cgtccgcgtc aacgttcacg agctcagcgt     300
cgagcagctc acagtctcgg agtacctccg cttcaaggag gagcttgtcg acggccagca     360
caatgatccc tacgttctcg agcttgactt cgagccgttc aatgtctcag tcccacgccc     420
aaatcggtca tcatctattg gaaacggtgt gcagttcctc aaccgacact tgtcctcaat     480
catgttccgc aacagggatt gcttggagcc cctgttggat ttcctccgtg gccaccggca     540
caaggggcat gttatgatgc ttaatgatag aatacaaagc ttggggaggc ttcagtctgt     600
gctgaccaaa gctgaggagc acttgtcaaa gctccctgct gacacaccat actcacaatt     660
tgcttataaa tttcaagagt ggggcctgga gaaaggttgg ggtgatacag caggacatgt     720
tttggaaatg atccatctcc ttctagacat cattcaggcg ccagacccat ctaccctaga     780
gaaattcttg gggaggatcc ccatgatttt taacgttgtt gtggtatccc ctcatggata     840
ctttggtcaa gctaatgtat taggcttgcc agacacagga ggacagatcg tctatatact     900
ggaccaagtc cgtgcactag aaaatgagat ggttctccgt ttaaagaaac aagggcttga     960
tgtttcccca aagattctca ttgttactcg gctgatacca gatgcaaaag gaacatcatg    1020
caatcagcgg cttgagagaa ttagtggaac acagcatact tacatattac gagttccctt    1080
cagaaatgaa aatgggatac ttaagaaatg gatatcaaga tttgatgtgt ggccatatct    1140
ggaaacattt gctgaggatg ctgctggtga aattgctgct gaattacaag gtactccaga    1200
cttcataatt ggaaactaca gtgatggaaa tcttgtggcg tcattgctat cttacaagat    1260
gggaattacc cagtgcaaca ttgctcatgc tctggaaaag actaagtatc cagattcaga    1320
catattttgg aagaatttcg atgagaagta ccatttctcc tgccagttca ctgctgatat    1380
aattgctatg aacaatgctg attttatcat caccagcaca taccaagaaa ttgctggaag    1440
caaaaatact gttggacagt atgagagtca tactgccttt actctgcctg tctgtaccg     1500
agttgtccat gggatcgatg tcttcgatcc aaagttcaat atagtctctc ctggagctga    1560
catgtccata tactttccac ataccgagaa ggccaagcga ctcacctctc ttcatggttc    1620
aatcgaaaat ttgatttatg acccggagca aaacgatgaa cacattgggc atctggatga    1680
ccggtcaaag cccatcctct tctccatggc aagactcgac agggtgaaga acataacagg    1740
gctggtcgaa gcttttgcta agtgcgctaa gctgagggag ctggtaaacc ttgtcgtcgt    1800
tgccgggtac aatgatgtca acaagtccaa ggacagggaa gagatcgcgg agatagagaa    1860
gatgcatgaa ctcatcaaga cccacaactt gttcgggcag ttccgctgga tctctgccca    1920
gacaaacagg gcccgtaacg gcgagctcta tcgctacatc gctgataccc atggtgcttt    1980
cgtacagccg gccttgtatg aagcgttcgg tctcaccgtc gttgaggcca tgacctgtgg    2040
gcttcctact ttcgcgacgc tccatggagg tccagctgag atcatagagc atggcgtctc    2100
gggcttccac attgacccgt accaccccga acaggctgtt aatctgatgg ccgacttctt    2160
cgaccggtgc aagcaagacc cagatcactg ggtgaatata tctggagcag ggctgcagcg    2220
catatacgag aagtacacat ggaagatata ctcagagagg ttgatgacac tggccggggt    2280
ctacggtttc tggaagtacg tgtcgaagct cgagaggctg gagacgaggc gctaccttga    2340
gatgttctac atactgaagt tccgcgagct ggcgaagacc gtgccgcttg caattgacca    2400
accgcagtag cttgcgcaac tgcgactgcg tagcacttgg tacaagactg aaacctgaag    2460
gaccttcagt aatttaggcg cggcagacgg tagccaataa aatgtgccgg agctgaactg    2520
gttttttatt atgtacataa tggcagtata acaaaattac tgaaggcagg tgggttgcag    2580
ttgtgtgttc gttactgttt actgtattat gtcaagctgt cggctgcaat ttctttgctg    2640
gcaagccgca ggcactggtg aagtgctgat aaatacatca tattctgttg acctgtgaaa    2700
aaaaaaaaaa aaaaaaaaaa aaaaaagggg cggccgc
```

Figure 11